WHAT IS CLAIMED IS:

1. A method of treating hypertrophy in a cardiomyocyte cell comprising the step of inhibiting the function of MEF2.

2. The method of claim 1, wherein inhibiting the function of MEF2 comprises reducing the expression of MEF2.

3. The method of claim 2, wherein inhibiting the function of MEF2 comprises contacting MEF2 with an agent that binds to and inactivates MEF2.

4. The method of claim 1, wherein said method further comprises inhibiting the upregulation of a gene upregulated by MEF2.

5. The method of claim 3, wherein the agent that reduces the expression of MEF2 is an antisense construct.

6. The method of claim 3, wherein the agent that binds to and inactivates MEF2 is an antibody preparation or a small molecule inhibitor.

7. The method of claim 6, wherein the antibody preparation comprises a single chain antibody.

8. The method of claim 6, wherein said antibody preparation consists essentially of a monoclonal antibody.

9. The method of claim 4, wherein the agent that inhibits the function of said genes is an antisense construct.

10. A transgenic, non-human mammal, the cells of which comprise an indicator gene under the control of a transcriptional regulatory element, wherein said transcriptional regulatory element is activated by MEF2.

11. The transgenic mammal of claim 10, wherein said mammal is a mouse.

12. The transgenic mammal of claim 10, wherein said indicator gene is selected from the group consisting of *lacZ*, a gene encoding green fluorescent protein and a gene encoding luciferase.

13. The transgenic mammal of claim 10, wherein said transcriptional regulatory element is a three tandem repeat of MEF2.

14. A method for screening modulators of cardiac hypertrophy comprising the steps of:

(a) providing a cardiomyocyte that contains an indicator gene under the control of MEF2-inducible regulatory sequences
(b) contacting said cell with a candidate modulator; and
(c) monitoring said cell for expression of said indicator gene as compared to a cell not treated with said candidate modulator.

15. The method of claim 14, wherein said cell is derived from a cardiomyocyte cell line.

16. The method of claim 14, wherein said cell is derived from a primary cardiomyocyte.

17. The method of claim 14, wherein contacting is performed *in vitro*.

18. The method of claim 14, wherein said contacting is performed *in vivo*.

19. The method of claim 14, wherein said cell is derived from a transgenic, non-human mammal.

20. The method of claim 14, wherein said candidate modulator is an antisense construct.

21. The method of claim 14, wherein said candidate modulator is from a small molecule library.

22. The method of claim 14, wherein said candidate modulator is an antibody.

23. The method of claim 22, wherein said antibody is a single chain antibody.

24. A method for identifying a gene involved in development of cardiac hypertrophy comprising the steps of:

(a) providing a cell having a MEF2 knockout;

(b) subjecting said cell to conditions leading to cardiac hypertrophy in a non-knockout cell of the same type;

(c) comparing the expression of genes in the MEF2 knockout cell with the expression of genes in the non-knockout cell; and

(d) identifying differentially expressed genes,

wherein genes differentially expressed are identified as involved in the development of cardiac hypertrophy.

25. The method of claim 24, further comprising comparing the differentially expressed genes of part (d) with genes expressed by a non-knockout cell in the absence of said conditions leading to cardiac hypertrophy.

26. The method of claim 24, wherein said comparing comprises subtraction hybridization.

27. The method of claim 24, wherein said comparing comprises PCR-mediated differential display.

28. An transcriptionally active MEF2 polypeptide comprising MEF2 fused to the transcriptional activation domain of an active transcription factor.

29. The polypeptide of claim 28, wherein said active transcription factor is VP16.

30. A polynucleotide encoding an transcriptionally active MEF2 molecule comprising a fusion of (a) MEF2 and (b) the transcriptional activation domain of an active transcription factor.

31. The polynucleotide of claim 30, wherein said active transcription factor is VP16.